

SEQUENCE LISTING

<110> Shionogi & Co., LTD.

<120> A gene encoding novel human secretory type  
phospholipase A2

<130> 51-06052W0

<150> JP 266616/1999

<151> 1999-09-21

<160> 34

<170> PatentIn Ver. 2.0

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<212> DNA

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gctatggcgc cctggagaan ctgggctgtg accccaagct ggaaaagtac ctcttctcta 180
tcactcgaga caacatcttc tgtgttgta aaacggcttg ccagcggcat acctgcgaat 240
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 aggtggcaga gcaggctccc atgccccctg cctacctccc ccagg atg aaa cct ccc 177  
 Met Lys Pro Pro  
 att gcc ctg gct tgc ctt tgc ctc ctg gtg ccc ctg gct ggc ggg aac 225  
 Ile Ala Leu Ala Cys Leu Cys Leu Leu Val Pro Leu Ala Gly Gly Asn  
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 Leu Gln Tyr Asn Asp Tyr Gly Cys Tyr Cys Gly Val Gly Gly Ser His  
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 tgg cca gtg gac gag acg gat tgg tgt tgt cat gcc cat gac tgc tgc 369  
 Trp Pro Val Asp Glu Thr Asp Trp Cys Cys His Ala His Asp Cys Cys  
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 Tyr Gly Arg Leu Glu Lys Leu Gly Cys Asp Pro Lys Leu Glu Lys Tyr  
 50 55 60 65  
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 Leu Phe Ser Ile Thr Arg Asp Asn Ile Phe Cys Ala Gly Arg Thr Ala  
 70 75 80  
 tgc cag cgg cat acc tgc gag tgt gac aag aga gct gct ctt tgc ttt 513  
 Cys Gln Arg His Thr Cys Glu Cys Asp Lys Arg Ala Ala Leu Cys Phe  
 85 90 95  
 cgc cac aac ctg aac act tac aac cgc aag tat gcc cac tac ccc aac 561  
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His Asp Cys Cys Tyr Gly Arg Leu Glu Lys Leu Gly Cys Asp Pro Lys  
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Leu Glu Lys Tyr Leu Phe Ser Ile Thr Arg Asp Asn Ile Phe Cys Ala  
           65                  70                  75

Gly Arg Thr Ala Cys Gln Arg His Thr Cys Glu Cys Asp Lys Arg Ala  
           80                  85                  90

Ala Leu Cys Phe Arg His Asn Leu Asn Thr Tyr Asn Arg Lys Tyr Ala  
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tcctgggaga aggaggggaag cctgggggca cctggaaaat tcaggctgat ctctcctctg 180  
ggctactttg ggctcnggg ccccgagcag ccctgggtcc agcccagcct ggctcacagg 240  
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Val Thr Gly Asn Leu Val Gln Phe Gly Val Met Ile Glu Lys Met Thr  
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ggc aag tcc gcc ctg cag tac aac gac tat ggc tgt tac tgc ggc atc 202  
Gly Lys Ser Ala Leu Gln Tyr Asn Asp Tyr Gly Cys Tyr Cys Gly Ile  
15 20 25

ggt ggc tcc cac tgg cgg gtg gac cag act gac tgg tgc tgc cac gcc 250  
Gly Gly Ser His Trp Pro Val Asp Gln Thr Asp Trp Cys Cys His Ala  
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cac gac tgc tgc tac ggg cgt ctg gag aag ctg ggc tgt gag ccc aaa 298  
His Asp Cys Cys Tyr Gly Arg Leu Glu Lys Leu Gly Cys Glu Pro Lys  
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ctg gaa aag tat ctt ttc tct gtc agc gaa cgt ggc att ttc tgc gcc 346  
Leu Glu Lys Tyr Leu Phe Ser Val Ser Glu Arg Gly Ile Phe Cys Ala  
65 70 75

ggc agg acc acc tgc cag cgg ctg acc tgc gag tgt gac aag agg gct 394  
Gly Arg Thr Thr Cys Gln Arg Leu Thr Cys Glu Cys Asp Lys Arg Ala  
80 85 90

gcc ctc tgc ttt cgc cgc aac ctg ggc acc tac aac cgc aaa tat gcc 442  
Ala Leu Cys Phe Arg Arg Asn Leu Gly Thr Tyr Asn Arg Lys Tyr Ala  
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Gly Lys Ser Ala Leu Gln Tyr Asn Asp Tyr Gly Cys Tyr Cys Gly Ile  
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Gly Gly Ser His Trp Pro Val Asp Gln Thr Asp Trp Cys Cys His Ala

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His Asp Cys Cys Tyr Gly Arg Leu Glu Lys Leu Gly Cys Glu Pro Lys			
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Leu Glu Lys Tyr Leu Phe Ser Val Ser Glu Arg Gly Ile Phe Cys Ala			
	65	70	75
Gly Arg Thr Thr Cys Gln Arg Leu Thr Cys Glu Cys Asp Lys Arg Ala			
	80	85	90
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<400> 34

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44